

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Barnwell, John
(ii) TITLE OF INVENTION: Plasmodium vivax Blood Stage Antigens,
Monoclonal Antibodies, and Diagnostic Assays

(iii) NUMBER OF SEQUENCES: 2

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Darby and Darby
(B) STREET: 805 Third Ave.
(C) CITY: New York
(D) STATE: New York
(E) COUNTRY: USA
(F) ZIP: 10022-7513

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: US
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Gogoris, Adda
(B) REGISTRATION NUMBER: 29,714
(C) REFERENCE/DOCKET NUMBER: 5986/07686

(viii) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (212)527-7700
(B) TELEFAX: (212)753-6237
(C) TELEX: 236687

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3337 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Plasmodium vivax

(vii) IMMEDIATE SOURCE:

(B) CLONE: PvMB3.3.1

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAATTCCGGT AAAGTAACAA CTATGGTTTC GTATCTATAT ATAACCTTAC TAATTTATC	60
TTTGCTTTT CTTTAATTC ATGCTTCAAC AGTAAGATAA AAATAATCTA TAAAAACTGC	120
TATATATACA TATATATTCA TAAGTGGCAT TTGTGAATTG CGATCATTTA AATTTACGTA	180
AAAACAATAT TGAAAAAAAT TTTTTTTTTT TTTTTTTTTT TGTTCTACAG AACGATTTAG	240
AATTGGAAAA TGCTTCTGAT GATGTTGTAG AGGTGGAGGA TCCTTCAAAC GACGGTTAG	300
AATTAGAAGA GGAAAATTG GATGAGAATT CAGGTGATGA TGAAACTCTT TTAGATGCTA	360
CCCCCGAAGA TGACTTTGCC TTAACAGATT TGCCAATTGA AGACGATGAG GAAGTCAACG	420
AAACGTTAGA TGGAGGTGAA TCATTAGGAG AGGTTCCAC TGAAGATATG GAAACAGAAG	480
ATGGCTAAC AGATGATACG GAAACAGAAG AAGGACTTACG TGGTGTATG GAAGGAGAAG	540
AAGAAGCTGG CGATATGGAA GCAGGGGAAG AAGCTGGTGA TTTGGAAGCA GGGGAAGAAA	600
CTGGCGATTT GGAAGCAGGG GAAGAAACTG GCGATTGGA AGCAGGGAA GAAGCTGGTG	660
ATTTGGAAAGC AGGGGAAGAA ACTGGCGATT TGGAAAGCAGG GGAAGAAACT GGAGATGCGG	720
AAACTGAAGA AGGAGCAACT GGAGATGCGG AAACTGAAAAA TGGAGCAACT GTGTATGTAG	780
ACACAGAAGA TAGTCAGCT GATGGAGCAG AAAAAGTACA TGTTCCTGCT CAAGAAAATG	840
TACAACCTGC CGATAGTAAT GATGCCCTCT TTGGAAGTAT TTTGGATAAA GATATAATT	900
TTGATCATAT TAAAGATTTC GAGCCACTAT TCGAACAAAT TGTGGCGGGT ACTGCTAAC	960
ATGTTACGGG ACAAGAATTG CCAATGAAAC CTGTACCATT ACCAGTGGCA GAAGAGCCCG	1020
CGCAAGTACC AGCGGAAGAA TTAGATGCCA CTCCAGAGGA TGACTTCGCA TTAGATGTTA	1080
CAGAATCTCC CGAGGAAGTA GAATTAGTAT TAGATGAAGA GGCAACTGAA GAAGAATCAA	1140
CGGAAGTGGG ACCAACGGAA GAAGGACCAA CCGAAGAATT AGATGCCACT CCAGAGGATG	1200
GATTCGCAT TAGACGAAAC TGCAGAAGGA GAAACAGAAG AAACGTAGAG GGAGAAGAAA	1260
CAGAAGAAGC TGCAGAAGGA GAAGTATCAG AAGAAACTCC AGAAGGAGAA GAAGAGTTAG	1320

AGGCAACTCC	AGAGGGATGAT	TTCGCATTAG	ATGGAAC TAC	ATTAGAAGAA	ACCGAAGAAA	1380
CTGCAGAAGG	AGAAGAAACC	GTAGAGGGAG	AAGAAACCGT	AGAGGGAGAA	GAAACCGTAG	1440
AGGGAGAAGA	AGCTGCAGAA	GGAGAAGAAG	AGTTAGAGGC	AACTCCAGAG	GATGACTTCC	1500
AATTAGAAGA	ACCATCAGGA	GAAGGAGAAG	GGGAAGGAGA	AGGAGAAGGG	GAAGGAGAAG	1560
GAGAAGCGTT	AGTAGCAGTG	CCAGTAGTGG	CCGAACCGGT	AGAAGTAGTG	ACTCCTGCTC	1620
AGCCTGTCAA	ACCAATGGTC	GCTCCAACGG	CAGATGAAAC	TTTATTGTT	GATATCTTAG	1680
ATAACGATT	AACGTATGCA	GACATTACAT	CCTTGAGCC	ATTATTTAAA	CAAATCCTCA	1740
AGGATCCTGA	TGCAGGGAGAG	GCTGTAACAG	TACCATCAAA	GGAAGCACCT	GTACAAGTAC	1800
CAGTGGCAGT	AGGGCCCGCG	CAAGAAGTGC	CAACGGAAGA	ATTGATGCAA	CTCCAAGAGG	1860
ACGATTTCGA	ATTAGAAGGA	ACTGCAGAAG	CTCCAGAGGA	AGGAGAATTA	GTATTAGAAG	1920
GAGAAGGAGA	ACCAACGGAA	GAAGAGCAA	GAGAAGGAGA	GCCAACAGAA	GGAGAAGTGC	1980
CAGA AA GAAGA	ATTAGAGGCA	ACTCCAGAGG	ACGATTTCGA	ATTAGAAGAA	CCAACAGGAG	2040
AAGA AA GTAGA	AGAAACCGTA	GAGGGCGAAG	AAACTGCAGA	AGGAGAAGAA	GTGGAAGAGG	2100
TACCTGCAGA	AGTAGAAGAA	GTGGAAGAGG	TACCTGCAGA	AGTAGAAGAA	GTGGAAGAGG	2160
TACCCAGAAGA	AGTAGAAGAG	GTACCCGCAG	AAGTAGAAGA	AGTGGAAAGAG	GTACCAGAAG	2220
AAGTGGAAAGA	GGTACCAAGAA	GAAGTGGAAAG	AGGTACCAAGA	AGAAGTGGAA	GAGGTACCAAG	2280
AAGA AA GTGGA	AGAAGTGGAA	GAAGTAGAAG	AAGTAGAGGT	ACCAGCGGTA	GTAGAAGTAG	2340
AAGTACCAAGC	GGTAGTAGAA	GAAGAGGTGC	CAGAAGAAGT	AGAAGAAGAA	GAAGAAGAGG	2400
AAGA AA CCAGT	AGAGGAAGAA	GATGTATTAC	AATTAGTAAT	ACCATCGGAA	GAAGATATAC	2460
AATTAGACAA	ACCAAAGAAA	GACGAATTAG	GCTCTGAAAT	TTTATCTATC	ATCGACATGC	2520
ACTACCAAGA	CGTTCCAAAG	GAATTATGG	AAGAAGAAGA	AGAAACTGCA	GTGTATCCAT	2580
TGAAACCAGA	AGATTTGCA	AAGGAAGATT	CACAATCTAC	AGAATGGCTC	ACATTCAATC	2640
AAGGCCTAGA	AGGCGACTGG	GAACGATTAG	AAGTGAGCTT	AAATAAGGCT	AGAGAAAGAT	2700
GGATGGAACA	AAGAAATAAA	GAATGGGCTG	GCTGGCTTCG	CTTAATTGAA	AATAAATGGT	2760
CAGAATATAG	TCAAATTCA	ACAAAAGGAA	AGGACCCAGC	TGGTTGAGA	AAACGAGAGT	2820
GGAGCGACGA	GAAATGGAAA	AAATGGTTA	AAGCAGAAGT	CAAATCCCAA	ATTGATTCAC	2880
ACTTGAAAAA	ATGGATGAAC	GACACTCATT	CCAATTATT	AAAATTCTT	GTGAAAGATA	2940

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TGTCACAATT TGAAAACAAG AAAACCAAAG AATGGTTAAT GAATCACTGG AAAAAGAACG 3000
AACGGGGTTA TGGTTCTGAA TCATTGAAAG TTATGACCAC ATCAAAATTA TTAAATGTGG 3060
CTAAGAGTCG AGAATGGTAC CGTGCCAATC CTAATATAAA TAGAGAAAGA AGAGAACTCA 3120
TGAAATGGTT TCTCCTAAAAA GAAAACGAAT ATTTAGGACA AAGAATGGAA AAAATGGACT 3180
CATTGGAAAA AAGTTAAATT TTTTGTGTTA AATTCAATGT GTACAACATT TTCTGGAAAA 3240
CGCCTAACCA AGGAAGAATG GAATCAATT GTTAATGAAA TAAAAGTTG AATTATAGAA 3300
AAAAGAACAG ATTATTCTCT TATAAAATAA ATAATTC 3337

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1018 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: C-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Plasmodium vivax

(vii) IMMEDIATE SOURCE:

- (B) CLONE: PvMB3.3.1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Asn Ser Gly Lys Val Thr Thr Met Val Ser Tyr Leu Tyr Ile Thr Leu
1 5 10 15

Leu Ile Leu Ser Phe Ala Phe Leu Leu Ile His Ala Ser Thr Asn Asp
20 25 30

Leu Glu Leu Glu Asn Ala Ser Asp Asp Val Val Glu Val Glu Asp Pro
35 40 45

Ser Asn Asp Gly Leu Glu Leu Glu Glu Asn Phe Asp Glu Asn Ser
50 55 60

Gly Asp Asp Glu Thr Leu Leu Asp Ala Thr Pro Glu Asp Asp Phe Ala
65 70 75 80

Leu Thr Asp Leu Pro Ile Glu Asp Asp Glu Glu Val Asn Glu Thr Leu

85	90	95
Asp Gly Gly Glu Ser Leu Gly Glu Val	Ser Thr Glu Asp Met Glu	Thr
100	105	110
Glu Asp Gly Ser Thr Asp Asp	Thr Glu Thr Glu Glu Gly	Leu Pro Gly
115	120	125
Asp Met Glu Gly Glu Glu Ala Gly Asp Met Glu	Ala Gly Glu Glu	
130	135	140
Ala Gly Asp Leu Glu Ala Gly Glu Glu Thr Gly	Asp Leu Glu Ala Gly	
145	150	160
Glu Glu Thr Gly Asp Leu Glu Ala Gly Glu Glu Ala Gly Asp Leu Glu		
165	170	175
Ala Gly Glu Glu Thr Gly Asp Leu Glu Ala Gly Glu Glu Thr Gly Asp		
180	185	190
Ala Glu Thr Glu Glu Gly Ala Thr Gly Asp Ala Glu Thr Glu Asn Gly		
195	200	205
Ala Thr Val Tyr Val Asp Thr Glu Asp Ser Ser Ala Asp Gly Ala Glu		
210	215	220
Lys Val His Val Pro Ala Gln Glu Asn Val Gln Pro Ala Asp Ser Asn		
225	230	240
Asp Ala Leu Phe Gly Ser Ile Leu Asp Lys Asp Ile Ile Phe Asp His		
245	250	255
Ile Lys Asp Phe Glu Pro Leu Phe Glu Gln Ile Val Ala Gly Thr Ala		
260	265	270
Lys His Val Thr Gly Gln Glu Leu Pro Met Lys Pro Val Pro Leu Pro		
275	280	285
Val Ala Glu Glu Pro Ala Gln Val Pro Ala Glu Glu Leu Asp Ala Thr		
290	295	300
Pro Glu Asp Asp Phe Ala Leu Asp Val Thr Glu Ser Pro Glu Glu Val		
305	310	320
Glu Leu Val Leu Asp Glu Glu Ala Thr Glu Glu Glu Ser Thr Glu Val		
325	330	335
Gly Pro Thr Glu Glu Gly Pro Thr Glu Glu Leu Asp Ala Thr Pro Glu		
340	345	350
Asp Gly Phe Arg Ile Arg Arg Asn Cys Arg Arg Arg Asn Arg Arg Asn		
355	360	365
Val Glu Gly Glu Glu Thr Glu Ala Ala Glu Gly Glu Val Ser Glu		

370 375 380
Glu Thr Pro Glu Gly Glu Glu Glu Leu Glu Ala Thr Pro Glu Asp Asp
385 390 395 400
Phe Ala Leu Asp Gly Thr Thr Leu Glu Glu Thr Glu Glu Thr Ala Glu
405 410 415
Gly Glu Glu Thr Val Glu Gly Glu Glu Thr Val Glu Gly Glu Glu Thr
420 425 430
Val Glu Gly Glu Glu Ala Ala Glu Gly Glu Glu Leu Glu Ala Thr
435 440 445
Pro Glu Asp Asp Phe Gln Leu Glu Glu Pro Ser Gly Glu Gly Glu Gly
450 455 460
Glu Gly Glu Gly Glu Gly Glu Gly Glu Ala Leu Val Ala Val
465 470 475 480
Pro Val Val Ala Glu Pro Val Glu Val Val Thr Pro Ala Gln Pro Val
485 490 495
Lys Pro Met Val Ala Pro Thr Ala Asp Glu Thr Leu Phe Val Asp Ile
500 505 510
Leu Asp Asn Asp Leu Thr Tyr Ala Asp Ile Thr Ser Phe Glu Pro Leu
515 520 525
Phe Lys Gln Ile Leu Lys Asp Pro Asp Ala Gly Glu Ala Val Thr Val
530 535 540
Pro Ser Lys Glu Ala Pro Val Gln Val Pro Val Ala Val Gly Pro Ala
545 550 555 560
Gln Glu Val Pro Thr Glu Glu Leu Met Gln Leu Gln Glu Asp Asp Phe
565 570 575
Glu Leu Glu Gly Thr Ala Glu Ala Pro Glu Glu Gly Glu Leu Val Leu
580 585 590
Glu Gly Glu Gly Glu Pro Thr Glu Glu Glu Pro Arg Glu Gly Glu Pro
595 600 605
Thr Glu Gly Glu Val Pro Glu Glu Glu Leu Glu Ala Thr Pro Glu Asp
610 615 620
Asp Phe Glu Leu Glu Glu Pro Thr Gly Glu Glu Val Glu Glu Thr Val
625 630 635 640
Glu Gly Glu Glu Thr Ala Glu Gly Glu Glu Val Glu Glu Val Pro Ala
645 650 655
Glu Val Glu Glu Val Glu Glu Val Pro Ala Glu Val Glu Glu Val Glu

660

665

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Glu Val Pro Glu Glu Val Glu Glu Val Pro Ala Glu Val Glu Glu Val
 675 680 685

Glu Glu Val Pro Glu Glu Val Glu Glu Val Pro Glu Glu Val Glu Glu
 690 695 700

Val Pro Glu Glu Val Glu Glu Val Pro Glu Glu Val Glu Glu Val Glu
 705 710 715 720

Glu Val Glu Glu Val Glu Val Pro Ala Val Val Glu Val Glu Val Pro
 725 730 735

Ala Val Val Glu Glu Val Pro Glu Glu Val Glu Glu Glu Glu Glu
 740 745 750

Glu Glu Glu Pro Val Glu Glu Glu Asp Val Leu Gln Leu Val Ile Pro
 755 760 765

Ser Glu Glu Asp Ile Gln Leu Asp Lys Pro Lys Lys Asp Glu Leu Gly
 770 775 780

Ser Gly Ile Leu Ser Ile Ile Asp Met His Tyr Gln Asp Val Pro Lys
 785 790 795 800

Glu Phe Met Glu Glu Glu Glu Glu Thr Ala Val Tyr Pro Leu Lys Pro
 805 810 815

Glu Asp Phe Ala Lys Glu Asp Ser Gln Ser Thr Glu Trp Leu Thr Phe
 820 825 830

Ile Gln Gly Leu Glu Gly Asp Trp Glu Arg Leu Glu Val Ser Leu Asn
 835 840 845

Lys Ala Arg Glu Arg Trp Met Glu Gln Arg Asn Lys Glu Trp Ala Gly
 850 855 860

Trp Leu Arg Leu Ile Glu Asn Lys Trp Ser Glu Tyr Ser Gln Ile Ser
 865 870 875 880

Thr Lys Gly Lys Asp Pro Ala Gly Leu Arg Lys Arg Glu Trp Ser Asp
 885 890 895

Glu Lys Trp Lys Lys Trp Phe Lys Ala Glu Val Lys Ser Gln Ile Asp
 900 905 910

Ser His Leu Lys Lys Trp Met Asn Asp Thr His Ser Asn Leu Phe Lys
 915 920 925

Ile Leu Val Lys Asp Met Ser Gln Phe Glu Asn Lys Lys Thr Lys Glu
 930 935 940

Trp Leu Met Asn His Trp Lys Lys Asn Glu Arg Gly Tyr Gly Ser Glu

945

955

960

Ser Phe Glu Val Met Thr Thr Ser Lys Leu Leu Asn Val Ala Lys Ser
965 970 975

Arg Glu Trp Tyr Arg Ala Asn Pro Asn Ile Asn Arg Glu Arg Arg Glu
980 985 990

Leu Met Lys Trp Phe Leu Leu Lys Glu Asn Glu Tyr Leu Gly Gln Arg
995 1000 1005

Met Glu Lys Met Asp Ser Leu Glu Lys Ser
1010 1015

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